

STIC-Biotech/ChemLib

From: Steadman, David (AU1652)  
Sent: Monday, March 13, 2006 6:49 AM  
To: STIC-Biotech/ChemLib  
Subject: 09/763,824 sequence search request

181992 mg  
RECEIVED  
MAR 13 2006  
(STIC)

NAME: David Steadman  
AU: 1656  
Date: 3/13/06  
Office: Remsen 2B05  
Mailbox: Remsen 3C70

**Please search the following sequence in commercial databases:**

- 1) Standard search of SEQ ID NO:37 against amino acid databases.
- 2) Standard search of SEQ ID NO:37 against nucleic acid databases.

*Please save results to diskette.*

Thank you very much.

David J. Steadman, Ph.D.  
Primary Examiner  
Art Unit 1656  
Protein Crystallography and Recombinant Enzymes  
Office: Remsen 2B05  
Mailbox: Remsen 3C70  
Phone: (571) 272-0942

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 15, 2006, 12:56:51 ; Search time 1241 Seconds  
(without alignments)  
1033.391 Million cell updates/sec

Title: US-09-763-824B-37  
Perfect score: 2836  
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKGGKSKL 550

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame\_plus\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US09763824/runat\_14032006\_110502\_557/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss05h  
-USER=US09763824\_@CGN\_1\_1\_431\_@runat\_14032006\_110502\_557 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq1:\*  
7: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq1:\*  
9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
11: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*  
12: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq4:\*

13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2836	100.0	1653	7	US-10-787-906-10	Sequence 10, Appl	
2	2836	100.0	1653	12	US-11-118-855-25	Sequence 25, Appl	
3	2836	100.0	5597	12	US-11-170-751-5	Sequence 5, Appli	
4	2836	100.0	6525	12	US-11-181-148-3	Sequence 3, Appli	
5	2836	100.0	7487	12	US-11-181-148-4	Sequence 4, Appli	
6	2833	99.9	5620	8	US-10-618-526-21	Sequence 21, Appl	
7	2812	99.2	4818	12	US-11-170-751-6	Sequence 6, Appli	
8	2812	99.2	5924	12	US-11-193-750-3	Sequence 3, Appli	
9	2812	99.2	5982	12	US-11-193-750-2	Sequence 2, Appli	
10	2812	99.2	8512	12	US-11-096-622-20	Sequence 20, Appl	
11	2812	99.2	8565	12	US-11-096-622-21	Sequence 21, Appl	
12	2779	98.0	14002	12	US-11-119-330-6	Sequence 6, Appli	
13	1951.5	68.8	1644	9	US-11-211-039-3	Sequence 3, Appli	
14	1951.5	68.8	1644	12	US-11-179-411-3	Sequence 3, Appli	
15	1951.5	68.8	1644	12	US-11-175-766-3	Sequence 3, Appli	
16	1893	66.7	1150	8	US-10-611-823-11	Sequence 11, Appl	
c 17	1068	37.7	2767	12	US-11-186-196-1	Sequence 1, Appli	
18	748	26.4	1653	9	US-11-096-568A-30774	Sequence 30774, A	
19	722	25.5	2767	12	US-11-186-196-1	Sequence 1, Appli	
20	680.5	24.0	1653	9	US-11-096-568A-29166	Sequence 29166, A	
21	680.5	24.0	1774	9	US-11-096-568A-34189	Sequence 34189, A	
22	644	22.7	1593	9	US-11-096-568A-30778	Sequence 30778, A	
23	591.5	20.9	1082144	12	US-11-117-187-211	Sequence 211, App	
24	487	17.2	1668	8	US-10-467-657-497	Sequence 497, App	
25	427	15.1	1632	7	US-10-932-182A-75619	Sequence 75619, A	
26	427	15.1	1632	7	US-10-932-182A-75619	Sequence 75619, A	
27	426.5	15.0	2206	8	US-10-510-386-67	Sequence 67, Appl	
28	422	14.9	1632	7	US-10-932-182A-227	Sequence 227, App	
29	422	14.9	1632	7	US-10-932-182A-227	Sequence 227, App	
30	390	13.8	1590	8	US-10-467-657-3803	Sequence 3803, Ap	
31	385.5	13.6	1848	9	US-11-096-568A-24055	Sequence 24055, A	
32	355.5	12.5	2235	7	US-10-932-182A-76276	Sequence 76276, A	
33	355.5	12.5	2235	7	US-10-932-182A-76276	Sequence 76276, A	
c 34	352.5	12.4	3049	8	US-10-793-626-4151	Sequence 4151, Ap	
35	351.5	12.4	3295	8	US-10-793-626-4049	Sequence 4049, Ap	
36	345	12.2	2313	9	US-11-096-568A-34453	Sequence 34453, A	
37	341.5	12.0	2085	7	US-10-932-182A-78109	Sequence 78109, A	
38	341.5	12.0	2085	7	US-10-932-182A-78109	Sequence 78109, A	
39	340	12.0	2235	7	US-10-932-182A-707	Sequence 707, App	
40	340	12.0	2235	7	US-10-932-182A-707	Sequence 707, App	
41	338.5	11.9	888	8	US-10-793-626-2945	Sequence 2945, Ap	
42	322.5	11.4	1203	8	US-10-793-626-2773	Sequence 2773, Ap	
43	322.5	11.4	3779	12	US-11-136-527-1866	Sequence 1866, Ap	
44	321	11.3	200	10	US-11-101-244-30	Sequence 30, Appl	
45	321	11.3	200	11	US-11-083-784-30	Sequence 30, Appl	

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 15, 2006, 12:33:45 ; Search time 8151 Seconds  
 (without alignments)  
 3835.591 Million cell updates/sec

Title: US-09-763-824B-37  
 Perfect score: 2836  
 Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGKSKL 550

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
 -Q=/abss/ABSSWEB\_spool/US09763824/runat\_14032006\_110454\_345/app\_query.fasta\_1  
 -DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h  
 -USER=US09763824\_CGN\_1\_1\_4939 @runat\_14032006\_110454\_345 -NCPU=6 -ICPU=3  
 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
 1: gb\_ba:\*  
 2: gb\_in:\*  
 3: gb\_env:\*  
 4: gb\_om:\*  
 5: gb\_ov:\*  
 6: gb\_pat:\*  
 7: gb\_ph:\*  
 8: gb\_pr:\*  
 9: gb\_ro:\*  
 10: gb\_sts:\*  
 11: gb\_sy:\*  
 12: gb\_un:\*  
 13: gb\_vi:\*  
 14: gb\_htg:\*  
 15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2836	100.0	1650	6	I66435	I66435 Sequence 1
	2	2836	100.0	1653	6	AX256409	AX256409 Sequence
	3	2836	100.0	1705	6	AX407020	AX407020 Sequence
	4	2836	100.0	1722	6	A84222	A84222 Sequence 1
	5	2836	100.0	1773	2	PP911ACNP	X84848 P.pyralis 1
	6	2836	100.0	1811	6	A37556	A37556 Sequence 22
	7	2836	100.0	2445	6	I46976	I46976 Sequence 8
	8	2836	100.0	3519	6	AR679362	AR679362 Sequence
	9	2836	100.0	3666	11	U66309	U66309 Expression
	10	2836	100.0	3891	11	U66311	U66311 Expression
	11	2836	100.0	3901	11	U66310	U66310 Expression
	12	2836	100.0	4544	6	AR232930	AR232930 Sequence
	13	2836	100.0	4672	6	AX701675	AX701675 Sequence
	14	2836	100.0	4672	11	CVE277960	AJ277960 Cloning v
	15	2836	100.0	4674	11	XXU02437	U02437 Cloning vec
c	16	2836	100.0	4931	11	CVPGEMLUC	X65316 Cloning vec
	17	2836	100.0	5051	6	AR643265	AR643265 Sequence
	18	2836	100.0	5067	11	AF093685	AF093685 Luciferas
	19	2836	100.0	5411	11	CVU03687	U03687 Photinus py
	20	2836	100.0	5499	11	AF093684	AF093684 Luciferas
	21	2836	100.0	5596	11	CVLUCLIC	U25266 Ligation-in
	22	2836	100.0	5598	11	CVPGL2BAS	X65323 Cloning vec
	23	2836	100.0	5675	11	AF053698	AF053698 Reporter
	24	2836	100.0	5688	11	AF053461	AF053461 Reporter
	25	2836	100.0	5695	11	AF053315	AF053315 Reporter
	26	2836	100.0	5714	11	AF167311	AF167311 Reporter
	27	2836	100.0	5743	11	AF053462	AF053462 Reporter
	28	2836	100.0	5748	11	AF058756	AF058756 Cloning v
	29	2836	100.0	5777	6	AX522061	AX522061 Sequence
	30	2836	100.0	5790	11	CVPGL2PRO	X65326 Cloning vec
	31	2836	100.0	5818	6	AR089207	AR089207 Sequence
	32	2836	100.0	5819	6	AR089206	AR089206 Sequence
	33	2836	100.0	5847	11	AF311601	AF311601 Reporter
	34	2836	100.0	5849	6	CQ815105	CQ815105 Sequence
	35	2836	100.0	5855	11	CVPGL2ENH	X65325 Cloning vec
	36	2836	100.0	5909	11	AF081837	AF081837 Cloning v
	37	2836	100.0	5938	6	AR089208	AR089208 Sequence
	38	2836	100.0	5969	11	AF434923	AF434923 Expressio
	39	2836	100.0	6044	6	I70203	I70203 Sequence 18
c	40	2836	100.0	6047	6	I70197	I70197 Sequence 12
	41	2836	100.0	6047	11	CVPGL2CON	X65324 Cloning vec
c	42	2836	100.0	6047	11	CVU40374	U40374 Luciferase
c	43	2836	100.0	6083	11	CVU89934	U89934 Cloning vec
	44	2836	100.0	6092	6	AR089205	AR089205 Sequence
	45	2836	100.0	6163	11	AF093682	AF093682 Luciferas

GenCore version 5.1.7

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 15, 2006, 01:41:50 ; Search time 1487 Seconds  
(without alignments)  
2465.085 Million cell updates/sec

Title: US-09-763-824B-37  
Perfect score: 2836  
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGKSKL 550

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US09763824/runat\_14032006\_110453\_328/app\_query.fasta\_1  
-DB=N\_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p  
-USER=US09763824\_@CGN\_1\_1\_1929\_@runat\_14032006\_110453\_328 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_21:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2836	100.0	1650	14	ADZ27248	Adz27248 Wild type
2	2836	100.0	1653	4	AAS15661	Aas15661 Luciferas
3	2836	100.0	1653	6	ABS68147	Abs68147 Luciferas
4	2836	100.0	1653	6	ABT08302	Abt08302 EcR-based
5	2836	100.0	1653	6	AAL49748	Aal49748 Firefly 1
6	2836	100.0	1653	6	ABS70116	Abs70116 Luciferas
7	2836	100.0	1653	12	ADH01021	Adh01021 Luciferas
8	2836	100.0	1653	12	ADH81003	Adh81003 Luciferas
9	2836	100.0	1653	13	ADR42616	Adr42616 Luciferas
10	2836	100.0	1653	13	ADR57978	Adr57978 Luciferas
11	2836	100.0	1653	13	ADR90410	Adr90410 Luciferas
12	2836	100.0	1705	6	ABK49460	Abk49460 Photinus
13	2836	100.0	1705	8	ACC00570	Acc00570 P. pyrali
14	2836	100.0	1705	9	ACF36063	Acf36063 Firefly 1
15	2836	100.0	1705	9	ACC71958	Acc71958 P. pyrali
16	2836	100.0	1722	2	AAX02223	Aax02223 P. pyrali
17	2836	100.0	1811	2	AAQ58732	Aaq58732 Encodes f
18	2836	100.0	3519	11	ADJ14195	Adj14195 N-termina
19	2836	100.0	3519	11	ADM18348	Adm18348 His6-BCCP
20	2836	100.0	4544	6	ABN86647	Abn86647 LUC-U3'-U
21	2836	100.0	4544	8	ABS57515	Abs57515 LUC-U3'-U
22	2836	100.0	4672	6	ABS55458	Abs55458 Chicken 1
23	2836	100.0	4846	2	AAV72416	Aav72416 P. pyrali
24	2836	100.0	5051	5	AAC86954	Aac86954 Nucleotid
25	2836	100.0	5427	4	AAC83390	Aac83390 Luciferas
26	2836	100.0	5620	2	AAT48630	Aat48630 Ad5-ITR,
27	2836	100.0	5620	4	AAF30233	Aaf30233 Minimal a
28	2836	100.0	5777	6	ABK91250	Abk91250 Plasmid t
29	2836	100.0	5789	2	AAX08779	Aax08779 pGL2-Prom
30	2836	100.0	5791	2	AAX08778	Aax08778 pGL2 (GST-
31	2836	100.0	5793	2	AAX08777	Aax08777 pGL2 (apo
32	2836	100.0	5793	2	AAX08776	Aax08776 pGL2 (apo
33	2836	100.0	5818	3	AAZ38352	Aaz38352 Plasmid p
34	2836	100.0	5819	2	AAX08774	Aax08774 pGL2 (apo
35	2836	100.0	5819	2	AAX08775	Aax08775 pGL2 (apo
36	2836	100.0	5819	3	AAZ38351	Aaz38351 Plasmid p
37	2836	100.0	5849	12	ADO43719	Ado43719 Nucleotid
38	2836	100.0	5938	3	AAZ38353	Aaz38353 Plasmid p
39	2836	100.0	6044	2	AAT28280	Aat28280 Plasmid p
40	2836	100.0	6092	2	AAX08773	Aax08773 pGL2 (apo
41	2836	100.0	6092	3	AAZ38350	Aaz38350 Plasmid p
42	2836	100.0	6170	2	AAQ98929	Aaq98929 Vector p1
43	2836	100.0	6171	2	AAT28279	Aat28279 Plasmid p
44	2836	100.0	6254	2	AAQ98916	Aaq98916 TGF-beta
45	2836	100.0	6464	2	AAQ98933	Aaq98933 Vector HB

GenCore version 5.1.7

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 15, 2006, 01:45:35 ; Search time 476 Seconds  
 (without alignments)  
 2053.905 Million cell updates/sec

Title: US-09-763-824B-37  
 Perfect score: 2836  
 Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGGKSKL 550

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
 -Q=/abss/ABSSWEB\_spool/US09763824/runat\_14032006\_110458\_452/app\_query.fasta\_1  
 -DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
 -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
 -HOST=abss02p -USER=US09763824\_CGN\_1\_1\_512@runat\_14032006\_110458\_452 -NCPUs=6  
 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
 7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
 8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

%  
 Result Query



No.	Score	Match	Length	DB	ID	Description
1	2836	100.0	1650	2	US-08-354-240A-1	Sequence 1, Appli
2	2836	100.0	1722	3	US-09-380-061B-1	Sequence 1, Appli
3	2836	100.0	1811	3	US-08-867-352-22	Sequence 22, Appl
4	2836	100.0	2445	2	US-08-122-520C-8	Sequence 8, Appli
5	2836	100.0	3519	3	US-10-154-515A-3	Sequence 3, Appli
6	2836	100.0	3519	3	US-10-122-706-3	Sequence 3, Appli
7	2836	100.0	4544	3	US-09-488-270A-1	Sequence 1, Appli
8	2836	100.0	5051	3	US-09-980-585A-1	Sequence 1, Appli
9	2836	100.0	5427	3	US-09-282-996-2	Sequence 2, Appli
10	2836	100.0	5789	3	US-08-862-431-32	Sequence 32, Appl
11	2836	100.0	5791	3	US-08-862-431-31	Sequence 31, Appl
12	2836	100.0	5793	3	US-08-862-431-29	Sequence 29, Appl
13	2836	100.0	5793	3	US-08-862-431-30	Sequence 30, Appl
14	2836	100.0	5818	2	US-08-536-559A-3	Sequence 3, Appli
15	2836	100.0	5819	2	US-08-536-559A-2	Sequence 2, Appli
16	2836	100.0	5819	3	US-08-862-431-27	Sequence 27, Appl
17	2836	100.0	5819	3	US-08-862-431-28	Sequence 28, Appl
18	2836	100.0	5938	2	US-08-536-559A-4	Sequence 4, Appli
19	2836	100.0	6044	2	US-08-316-950-18	Sequence 18, Appl
20	2836	100.0	6044	6	PCT-US95-12642-18	Sequence 18, Appl
c 21	2836	100.0	6047	2	US-08-316-950-12	Sequence 12, Appl
c 22	2836	100.0	6047	6	PCT-US95-12642-12	Sequence 12, Appl
23	2836	100.0	6092	2	US-08-536-559A-1	Sequence 1, Appli
24	2836	100.0	6092	3	US-08-862-431-26	Sequence 26, Appl
25	2836	100.0	6171	2	US-08-316-950-17	Sequence 17, Appl
26	2836	100.0	6171	6	PCT-US95-12642-17	Sequence 17, Appl
27	2836	100.0	8937	3	US-09-872-733A-8	Sequence 8, Appli
28	2836	100.0	8937	3	US-09-872-733A-9	Sequence 9, Appli
29	2836	100.0	11616	2	US-08-196-259-2	Sequence 2, Appli
30	2833	99.9	5405	3	US-09-282-996-1	Sequence 1, Appli
31	2833	99.9	5620	2	US-08-793-170-21	Sequence 21, Appl
32	2833	99.9	5620	3	US-08-892-873-21	Sequence 21, Appl
33	2833	99.9	5620	3	US-09-334-765A-21	Sequence 21, Appl
34	2833	99.9	5620	3	US-09-356-575E-21	Sequence 21, Appl
35	2833	99.9	5620	3	US-09-333-820-21	Sequence 21, Appl
36	2833	99.9	5620	3	US-09-506-548A-21	Sequence 21, Appl
37	2833	99.9	5620	3	US-09-912-552-21	Sequence 21, Appl
38	2833	99.9	5620	3	US-09-918-029-21	Sequence 21, Appl
39	2830	99.8	1722	3	US-08-718-425-1	Sequence 1, Appli
40	2830	99.8	10160	3	US-09-097-319A-8	Sequence 8, Appli
41	2830	99.8	10160	3	US-09-643-971-8	Sequence 8, Appli
42	2830	99.8	11784	3	US-09-097-319A-9	Sequence 9, Appli
43	2830	99.8	11784	3	US-09-643-971-9	Sequence 9, Appli
44	2830	99.8	11991	3	US-09-097-319A-10	Sequence 10, Appl
45	2830	99.8	11991	3	US-09-643-971-10	Sequence 10, Appl

GenCore version 5.1.7

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 15, 2006, 12:47:09 ; Search time 1238 Seconds  
(without alignments)  
3673.795 Million cell updates/sec

Title: US-09-763-824B-37  
Perfect score: 2836  
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGGKSKL 550

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US09763824/runat\_14032006\_110500\_504/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_Main -QFMT=fastap -SUFFIX=p2n.rnpbm  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext  
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h  
-USER=US09763824@CGN\_1\_1\_1026@runat\_14032006\_110500\_504 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	2836	100.0	1650	9	US-10-954-840-5	Sequence 5, Appli	
2	2836	100.0	1653	3	US-09-965-703-66	Sequence 66, Appl	
3	2836	100.0	1653	7	US-10-239-134-57	Sequence 57, Appl	
4	2836	100.0	1653	7	US-10-614-116-9	Sequence 9, Appli	
5	2836	100.0	1653	7	US-10-468-199-62	Sequence 62, Appl	
6	2836	100.0	1653	7	US-10-783-810-10	Sequence 10, Appl	
7	2836	100.0	1653	9	US-10-775-883-10	Sequence 10, Appl	
8	2836	100.0	1653	9	US-10-460-820-9	Sequence 9, Appli	
9	2836	100.0	1705	3	US-09-965-697-13	Sequence 13, Appl	
10	2836	100.0	1705	8	US-10-490-971-22	Sequence 22, Appl	
11	2836	100.0	1705	8	US-10-490-976-25	Sequence 25, Appl	
12	2836	100.0	3519	5	US-10-122-706-3	Sequence 3, Appli	
13	2836	100.0	3519	9	US-10-494-073-3	Sequence 3, Appli	
14	2836	100.0	4672	5	US-10-059-561-5	Sequence 5, Appli	
15	2836	100.0	5777	8	US-10-467-781A-3	Sequence 3, Appli	
16	2836	100.0	5849	8	US-10-677-777-1	Sequence 1, Appli	
17	2836	100.0	6525	5	US-10-055-794-3	Sequence 3, Appli	
18	2836	100.0	6565	3	US-09-957-458B-4	Sequence 4, Appli	
19	2836	100.0	6971	3	US-09-957-458B-2	Sequence 2, Appli	
20	2836	100.0	7487	5	US-10-055-794-4	Sequence 4, Appli	
21	2836	100.0	7558	3	US-09-957-458B-3	Sequence 3, Appli	
22	2836	100.0	7969	3	US-09-957-458B-1	Sequence 1, Appli	
23	2836	100.0	8937	3	US-09-872-733-8	Sequence 8, Appli	
24	2836	100.0	8937	3	US-09-872-733-9	Sequence 9, Appli	
25	2836	100.0	8937	5	US-10-263-020-8	Sequence 8, Appli	
26	2836	100.0	8937	5	US-10-263-020-9	Sequence 9, Appli	
27	2836	100.0	8937	7	US-10-644-027-8	Sequence 8, Appli	
28	2836	100.0	8937	7	US-10-644-027-9	Sequence 9, Appli	
29	2836	100.0	36083	9	US-10-944-496-21	Sequence 21, Appl	
30	2833	99.9	5620	3	US-09-918-029-21	Sequence 21, Appl	
31	2833	99.9	5620	3	US-09-912-552-21	Sequence 21, Appl	
32	2833	99.9	5620	5	US-10-038-271-21	Sequence 21, Appl	
33	2833	99.9	5620	5	US-10-125-751-21	Sequence 21, Appl	
34	2833	99.9	5620	5	US-10-219-414-21	Sequence 21, Appl	
35	2833	99.9	5620	8	US-10-850-140-21	Sequence 21, Appl	
36	2832	99.9	2502	6	US-10-220-262-8	Sequence 8, Appli	
37	2830	99.8	10160	7	US-10-759-602-8	Sequence 8, Appli	
38	2830	99.8	11784	7	US-10-759-602-9	Sequence 9, Appli	
39	2830	99.8	11991	7	US-10-759-602-10	Sequence 10, Appl	
40	2829	99.8	1650	9	US-10-954-840-1	Sequence 1, Appli	
c 41	2825	99.6	5313	7	US-10-688-299-48	Sequence 48, Appl	
42	2825	99.6	10769	7	US-10-688-299-46	Sequence 46, Appl	
43	2820	99.4	1650	9	US-10-954-840-3	Sequence 3, Appli	
44	2818	99.4	1814	3	US-09-967-107B-8	Sequence 8, Appli	
45	2812	99.2	1651	7	US-10-332-733-27	Sequence 27, Appl	

- GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 15, 2006, 12:38:05 ; Search time 6209 Seconds  
(without alignments)  
4144.451 Million cell updates/sec

Title: US-09-763-824B-37  
Perfect score: 2836  
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGKSKL 550

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US09763824/runat\_14032006\_110456\_390/app\_query.fasta\_1  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h  
-USER=US09763824@CGN\_1\_1\_5315@runat\_14032006\_110456\_390 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_htc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.		%					
	1	1748	61.6	1034	9	BZ676934	BZ676934 PUBIF45TD
c	2	1739	61.3	1032	9	BZ675132	BZ675132 PUBIG87TD
	3	1624	57.3	973	9	BZ701200	BZ701200 PUBMP50TD
	4	1617	57.0	944	9	BZ672965	BZ672965 PUBGD25TD
	5	1604	56.6	949	9	BZ681727	BZ681727 PUBHI42TD
c	6	1592	56.1	929	9	BZ678861	BZ678861 PUBFK69TD
c	7	1587	56.0	911	9	BZ671975	BZ671975 PUBEX85TD
	8	1550	54.7	902	9	BZ670418	BZ670418 PUBEN17TD
	9	1532	54.0	916	9	BZ679896	BZ679896 PUBEV13TD
c	10	1520	53.6	885	9	BZ686758	BZ686758 PUBFE30TD
c	11	1513	53.3	884	9	BZ703458	BZ703458 PUBLO07TD
	12	1490	52.5	866	9	BZ682015	BZ682015 PUBJP02TD
c	13	1488	52.5	882	9	BZ682835	BZ682835 PUBGP67TD
	14	1481	52.2	892	9	BZ677942	BZ677942 PUBFU55TD
	15	1469	51.8	867	9	BZ683904	BZ683904 PUBHO53TD
c	16	1450	51.1	863	9	BZ676173	BZ676173 PUBHT60TD
c	17	1410	49.7	822	9	BZ682928	BZ682928 PUBHQ02TD
	18	1393	49.1	814	9	BZ685628	BZ685628 PUBFI19TD
	19	1390	49.0	811	9	BZ676058	BZ676058 PUBFD85TD
	20	1373	48.4	796	9	BZ669209	BZ669209 PUBCL07TD
c	21	1371	48.3	811	9	BZ687372	BZ687372 PUBHF61TD
c	22	1364	48.1	805	9	BZ702755	BZ702755 PUBMR69TD
c	23	1354	47.7	789	9	BZ669225	BZ669225 PUBDK64TD
	24	1337	47.1	796	9	BZ994546	BZ994546 PUBKI46TD
	25	1321	46.6	841	9	BZ669574	BZ669574 PUBCO87TD
	26	1304	46.0	760	9	BZ677712	BZ677712 PUBFD21TD
	27	1217.5	42.9	882	10	CW799568	CW799568 WiscDsLox
	28	1177	41.5	687	9	BZ683170	BZ683170 PUBCO64TD
	29	1119	39.5	659	6	CB546382	CB546382 AMGNNUC:N
c	30	1103	38.9	664	10	CL279934	CL279934 Ggal_143c
	31	1078	38.0	637	9	BZ670807	BZ670807 PUBBC62TD
	32	1047	36.9	618	6	CB579321	CB579321 AMGNNUC:N
c	33	1029	36.3	603	9	BZ700921	BZ700921 PUBLI28TD
	34	977	34.4	574	6	CB608609	CB608609 AMGNNUC:N
	35	932	32.9	541	6	CB612562	CB612562 AMGNNUC:N
c	36	917	32.3	855	9	BZ756044	BZ756044 PUBDL24TB
	37	902	31.8	777	10	CW803033	CW803033 WiscDsLox
	38	899	31.7	785	9	BZ684886	BZ684886 PUBFN18TD
	39	888	31.3	934	9	BZ677304	BZ677304 PUBGB93TD
	40	853	30.1	497	9	BZ683468	BZ683468 PUBBD76TD
	41	852	30.0	501	9	BZ701708	BZ701708 PUBMQ56TD
c	42	834	29.4	492	9	BZ684949	BZ684949 PUBCH20TD
	43	809.5	28.5	1832	4	CNS0ADI2	BX814596 Arabidops
	44	807.5	28.5	1825	4	CNS0ADOY	BX814621 Arabidops
	45	779.5	27.5	1833	4	CNS0A10J	BX832101 Arabidops